called Prime that can aid in selecting primers from a given template sequence. Protocols for the design and optimization of PCR reactions are commonly known in the art and are described in Saiki et al., *Science* 239:487 (1988); *Recombinant DNA Methodology*, Wu et al., eds., Academic Press, Inc., San Diego (1989), pp. 189-196; and PCR Protocols: *A Guide to Methods and Applications*, Innis et al., eds., Academic Press, Inc. (1990).

Antisense Nucleic Acid Molecules

[062] Other useful fragments of the nucleic acids include antisense or sense oligonucleotides comprising a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment of DNA from any one of SEQ ID NO: 1 through SEQ ID NO: 327. Such a fragment generally comprises at least about 14 nucleotides, preferably from about 14 to about 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (*Cancer Res.* 48:2659, 1988) and van der Krol et al. (*Bio/Techniques* 6:958, 1988).

[063] Binding of antisense or sense oligonucleotides to target nucleic acid sequences results in the formation of duplexes or other nucleic acid complexes inimical to efficient production of gene products. The antisense oligonucleotides thus may be used to block expression of proteins or the function of RNA. Antisense or sense oligonucleotides further comprise oligonucleotides having modified sugar-phosphodiester backbones (or other sugar linkages, such as those described in

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WO91/06629) and wherein such sugar linkages are resistant to endogenous nucleases. Such oligonucleotides with resistant sugar linkages are stable *in vivo* (i.e., capable of resisting enzymatic degradation) but retain sufficient sequence specificity to be able to bind to target nucleotide sequences.

[064] Other examples of sense or antisense oligonucleotides include those oligonucleotides which are covalently linked to organic moieties, such as those described in WO 90/10448, and other moieties that increases affinity of the oligonucleotide for a target nucleic acid sequence, such as poly-(L-lysine). Further still, intercalating agents, such as ellipticine, and alkylating agents or metal complexes may be attached to sense or antisense oligonucleotides. Such modifications may modify binding specificities of the antisense or sense oligonucleotide for the target nucleotide sequence.

[065] Antisense or sense oligonucleotides may be introduced into a cell containing the target nucleic acid sequence by any gene transfer method, including, for example, lipofection, $CaPO^4$-mediated DNA transfection, electroporation, or by using gene transfer vectors such as Epstein-Barr virus or adenovirus.

[066] Sense or antisense oligonucleotides also may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. In one embodiment, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand

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binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell.

[067] Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. The sense or antisense oligonucleotide-lipid complex is preferably dissociated within the cell by an endogenous lipase.

Polypeptides Encoded by Differentially-Expressed cDNAs

[068] The cDNAs of SEQ ID NOS: 1-327 can be translated into amino acid sequences potentially corresponding to portions of developmentally-regulated plant proteins. These amino acid sequences can be identified from sequences listed in Table I, below. The cDNAs encoding these predicted polypeptides are grouped into early, middle, and late transcripts according to the staged embryo population from which they were derived.

(See Table I)

[069] Although the term "peptide" is generally understood to reference synthetic sequences, or fragments of larger proteins, and includes short amino acid sequences of between 2 and 10 amino acids, whereas "polypeptide" refers to larger sequences and full-length proteins, the terms are used interchangeably herein to indicate that the invention applies to peptides and polypeptides of any length and variants thereof. Moreover, the discovery of presumptive open reading frames in SEQ ID NOS: 1-327, and the ability to isolate additional cDNA sequence, enables the construction of expression vectors comprising nucleic acid sequences encoding those polypeptides.